are highly homologous and the OG12X and Og12x proteins are 100% identical. In **situ hybridization** on mouse embryos ranging from 9 to 16 days post-coitum **localized** murine Og12x **mRNA** in the heart, otic region, maxillary and mandibular components of the first branchial arch, nasal processes, eyelid, midbrain, medulla oblongata, limbs, dorsal root ganglia and genital tubercle. OG12X was mapped to human chromosome 3q22-26 and murine Og12x to the syntenic region on mouse chromosome 3. Based upon the expression pattern of its mouse cognate, OG12X represents a candidate for the blepharophimosis (BPES) and Cornelia de Lange syndromes previously mapped to this region.

L21 ANSWER 9 OF 12 MEDLINE on STN
ACCESSION NUMBER: 1998201605 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9524245
TITLE: Structure and hair follicle-specific expression of genes encoding the rat high sulfur protein B2 family.
AUTHOR: Mitsui S; Ohuchi A; Adachi-Yamada T; Hotta M; Tsuboi R; Ogawa H
CORPORATE SOURCE: Kao Biological Science Laboratories, Tochigi, Japan.. smitsui@koto.kpu-m.ac.jp
SOURCE: Gene, (1998 Feb 27) 208 (2) 123-9.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB003753
ENTRY MONTH: 199805
ENTRY DATE: Entered STN: 19980514
Last Updated on STN: 20021018
Entered Medline: 19980504

AB High sulfur proteins are cysteine-rich proteins synthesized during the differentiation of hair matrix cells, and form hair fibers in association with hair keratin intermediate filaments. Rat high sulfur protein B2 **genes** were isolated after **screening** of a rat genomic library using the cDNA as a **probe**. Sequence analysis of a 4 kb fragment revealed two high sulfur protein genes, B2E and B2F. Both genes lacked introns, with B2F being located at 2 kb downstream of B2E. The 5' flanking regions of both genes had TATA and CAAT boxes, and consensus sequences of B2 genes. The upstream region of B2F had possible AP-1 and Sp-1 binding elements. The high sulfur protein B2E and B2F, which have putative 188 and 122 amino acids, respectively, comprised four distinct domains with a characteristic repetitive sequence. In **situ hybridization** indicated that the **mRNA** of high sulfur protein B2 was specifically **localized** in the cortex of the hair shaft, and northern blot analysis indicated that the expression of B2 increased in anagen and decreased in telogen, suggesting that high sulfur protein B2 synthesized in cortical cells during anagen contributes to the production of hair fibers.

L21 ANSWER 10 OF 12 MEDLINE on STN
ACCESSION NUMBER: 96044445 MEDLINE
DOCUMENT NUMBER: PubMed ID: 7558005
TITLE: Structure and chromosomal **localization** of a human water channel (AQP3) gene.
COMMENT: Erratum in: Genomics 1995 Dec 10;30(3):633
AUTHOR: Ishibashi K; Sasaki S; Saito F; Ikeuchi T; Marumo F
CORPORATE SOURCE: Second Department of Internal Medicine, School of Medicine, Tokyo, Japan.
SOURCE: Genomics, (1995 May 20) 27 (2) 352-4.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English

FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-D25280
ENTRY MONTH: 199511
ENTRY DATE: Entered STN: 19951227
Last Updated on STN: 19980206
Entered Medline: 19951113

AB A cDNA encoding rat AQP3, a water channel and a member of the MIP family, that is expressed predominantly in kidney medulla and colon was cloned recently. To determine the structure, tissue distribution, and chromosomal **localization** of the human AQP3 **gene**, we **screened** a human kidney cDNA library with rat AQP3 **probe** and isolated a cDNA coding for human AQP3 protein. The deduced amino acid sequence of human AQP3 was 91% identical to rat AQP3. Human AQP3 **mRNA** was expressed in colon, kidney, liver, pancreas, lung, peripheral leukocytes, spleen, and prostate. The human AQP3 gene was mapped to 7q36.2-q36.3 by chromosome fluorescence in **situ hybridization**.

L21 ANSWER 11 OF 12 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN
ACCESSION NUMBER: 90011858 EMBASE
DOCUMENT NUMBER: 1990011858
TITLE: **Localization** of urokinase-type and tissue-type plasminogen activator **mRNA** during organogenesis in the mouse.
AUTHOR: Menoud P.-A.; Debrot S.; Schowing J.
CORPORATE SOURCE: Institute of Zoology, Dept. Experim. Embryology, University of Fribourg,CH-1700 Fribourg, Switzerland
SOURCE: Roux's Archives of Developmental Biology, (1989) 198/4 (219-226).
ISSN: 0930-035X CODEN: WRABDT
COUNTRY: Germany
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 001 Anatomy, Anthropology, Embryology and Histology
021 Developmental Biology and Teratology
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Cryostat sections of E8.5 to E9.5 mouse embryos were hybridized with 35S-labelled RNA probes to urokinase-type and tissue-type plasminogen activator (uPA and tPA, respectively) **mRNA**. The sections were **screened** for expression of either **gene**. Two main features emerge from the results. (a) The stage of initial detection is different for each transcript. The uPA **mRNA** is first detected in cephalic mesenchyme at E8.5 when tPA **mRNA** is already widely distributed in tissues derived from ectoderm and mesoderm; later, the uPA **mRNA** transcripts were found throughout most mesodermic tissues. (b) Each gene presents a different pattern of expression. The uPA is restricted to single cells or to small groups of cells within tissues; this distribution suggests its involvement in cell migratory mechanisms. On the other hand, tPA was detected in most tissues, with variable intensities. Its expression gains complexity while organogenesis proceeds. This pattern supports the hypothesis that regulatory mechanisms other than a direct gene regulation are involved. In extraembryonic tissues, uPA and tPA genes are constantly expressed at a high level in trophoblastic giant cells and parietal endoderm, respectively. Our results confirm the presence of plasminogen activator during embryonic development and provide detailed picture of the plasminogen activator gene expression in mouse organogenesis.

L21 ANSWER 12 OF 12 MEDLINE on STN
ACCESSION NUMBER: 88210273 MEDLINE
DOCUMENT NUMBER: PubMed ID: 3365686
TITLE: Molecular cloning and characterization of an antigen associated with early stages of melanoma tumor progression.

THE GENUINE ARTICLE: FE826
TITLE: A DIURNAL-VARIATION OF VASOACTIVE-INTESTINAL-PEPTIDE (VIP) MESSENGER-RNA UNDER A DAILY LIGHT-DARK CYCLE IN THE RAT SUPRACHIASMATIC NUCLEUS

AUTHOR: OKAMOTO S; OKAMURA H; MIYAKE M; **TAKAHASHI Y**; TAKAGI S; AKAGI Y; FUKUI K; OKAMOTO H; IBATA Y (Reprint)

CORPORATE SOURCE: KYOTO PREFECTURAL UNIV MED, DEPT ANAT, KYOTO 602, JAPAN; KYOTO PREFECTURAL UNIV MED, DEPT OPHTHALMOL, KYOTO 602, JAPAN; KYOTO PREFECTURAL UNIV MED, DEPT PSYCHIAT, KYOTO 602, JAPAN; TOHOKU UNIV, SCH MED, DEPT BIOCHEM, SENDAI, MIYAGI 980, JAPAN

COUNTRY OF AUTHOR: JAPAN

SOURCE: HISTOCHEMISTRY, (1991) Vol. 95, No. 5, pp. 525-528.

DOCUMENT TYPE: Article; Journal

FILE SEGMENT: LIFE

LANGUAGE: ENGLISH

REFERENCE COUNT: 22



AB We detected a diurnal change of vasoactive intestinal peptide (VIP) messenger RNA (**mRNA**) in the rat suprachiasmatic nucleus (SCN) using the in **situ hybridization** technique combined with computed image analysis. The amount of VIP **mRNA** was greatest at 02.00 h, the next largest level was seen at 20.00 h during the dark phase and smallest at 14.00 h during the light phase. We also confirmed that the onset of the fluctuation of **mRNA** occurred 2-6 h prior to the diurnal variation of the content of VIP-like immunoreactivity by semiquantitative immunocytochemistry. These findings suggest that light stimulus from the retina is a primarily influence on the transcription of VIP **mRNA** and induces a diurnal variation of VIP synthesis.

LANGUAGE: English
ENTRY DATE: Entered STN: 17 Oct 2001
Last Updated on STN: 23 Feb 2002

AB The neuropeptide galanin is markedly up-regulated in dorsal root ganglia (DRG) at both the **mRNA** and protein levels following sciatic nerve transection (axotomy). It has been suggested that this upregulation may be an adaptive response involved in reducing neuropathic pain, or in promoting neuronal survival and regeneration. To date, three galanin G-protein-coupled receptors have been characterized, and we have recently used galanin knockout mice to demonstrate that galanin is a neurotrophic factor for adult regenerating sensory neurons (Holmes et al., 2000). Using suppression subtractive hybridization we have compared the **mRNA** expression in DRG seven days after axotomy in wild-type (WT) mice, to that in galanin knockout (KO) mice. The resulting putative differentially expressed **genes** were then **screened** by in **situ hybridization**, resulting in the identification of 'clone 960'. Expression of 'clone 960' **mRNA** decreased in WT DRG following axotomy, whereas it increased in KO DRG, such that post-axotomy expression in the KO was greater than WT. By Northern blot analysis the 2 kb transcript is moderately abundant in brain, and in **situ hybridization** demonstrates regional **localization**. We are currently cloning the full length cDNA corresponding to 'clone 960'. In-conclusion, we have isolated a cDNA that is differentially regulated in the DRG of WT and galanin KO mice following axotomy, which may contribute to the role of galanin in the nerve cell body response to peripheral nerve injury.

L16 ANSWER 18 OF 38 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
ACCESSION NUMBER: 2002:210665 BIOSIS
DOCUMENT NUMBER: PREV200200210665
TITLE: Chromosomal distribution, **localization** and expression of the human endogenous retrovirus ERV9.
AUTHOR(S): Svensson, A.-C.; Raudsepp, T.; Larsson, C.; Di Cristofano, A.; Chowdhary, B.; La Mantia, G.; Rask, L.; Andersson, G. [Reprint author]
CORPORATE SOURCE: Department of Animal Breeding and Genetics, Upsala Biomedical Center, Swedish University of Agricultural Sciences, S-751 24, Upsala, Sweden
Goran.Andersson@bmc.uu.se
SOURCE: Cytogenetics and Cell Genetics, (2001) Vol. 92, No. 1-2, pp. 89-96. print.
CODEN: CGCGBR. ISSN: 0301-0171.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 27 Mar 2002
Last Updated on STN: 27 Mar 2002

AB ERV9 is a class I family of human endogenous retroviral sequences. Somatic cell hybrid genomic hybridization experiments using a mono-chromosomal panel indicate the presence of approximately 120 ERV9 loci in the human genome distributed on most chromosomes. Fluorescence in **situ hybridization** (FISH) using an ERV9 cDNA probe containing gag, pol and env sequences, verified this observation and a consistent signal was found at the chromosome region 11q13.3 fwdarw q13.5. By analysis of a panel of radiation hybrids, an ERV9 locus was mapped to within a 300-kbp region at the chromosome site 11q13. The marker cCLGW567 and the locus MAP3K11/D11S546 centromeric and telomeric flanked it, respectively. Northern blot analysis, using an ERV9 LTR probe, indicated that most normal tissues examined expressed low abundant ERV9 LTR driven mRNAs of various sizes. The most prominent expression was found in adrenal glands and testis. However, the level of expression varied in the same tissues among different individuals indicating that ERV9 **mRNA** expression probably is inducible in certain tissues or at various cell stages.

L16 ANSWER 19 OF 38 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN

ACCESSION NUMBER: 2000172861 EMBASE
TITLE: Plasma membrane calcium pump isoform 1 gene expression is repressed by cortircosterone and stress in rat hippocampus.
AUTHOR: Bhargava A.; Meijer O.C.; Dallman M.F.; Pearce D.
CORPORATE SOURCE: Dr. D. Pearce, Department of Medicine, Box 0532, University of California, Parnassus Avenue, San Francisco, CA 94143, United States. pearced@medicine.ucsf.edu
SOURCE: Journal of Neuroscience, (1 May 2000) 20/9 (3129-3138). Refs: 60
ISSN: 0270-6474 CODEN: JNRSDS
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 002 Physiology
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Glucocorticoids (GCs) are critical to learning and memory, in large part because of their actions in the hippocampus. Chronic high levels of GCs have profound effects on hippocampal structure and function and can even result in irreversible neurodegeneration. Hippocampal GC actions are mediated by intracellular receptors that modulate the transcription of specific target **genes**. In a **screen** for **genes** repressed by GCs in rat hippocampus, we identified plasma membrane calcium pump isoform 1 (PMCA1), a plasma membrane calcium ATPase. In Northern blots, PMCA1 was repressed .apprx.33% after a high, but not a low dose of the GC, corticosterone (B), suggesting glucocorticoid (but not mineralocorticoid) receptor-mediated repression. Furthermore, in **situ hybridization** demonstrated that B significantly downregulated PMCA1 **mRNA** in all brain regions examined. Repression of PMCA1 was also observed in cultured hippocampal neurons, but only when the cells were in the differentiated state. Stress also repressed PMCA1 expression in hippocampus of adrenal-intact animals, and a clear inverse correlation between B level and PMCA1 **mRNA** could be discerned. However, other non-B-dependent factors appeared to be involved in the response of PMCA1 to stress because, unlike exogenous B, cold stress did not repress PMCA1 in brain regions other than hippocampus. Moreover, in the presence of constant B (B-replaced, adrenalectomized animals), cold stress led to increased hippocampal PMCA1 expression. These observations suggest that repression of PMCA1 represents one molecular mechanism by which corticosteroids regulate Ca2+ homeostasis and hence influence neuronal activity. Moreover, other stress-related neurohumoral factors appear to counter the repressive effects of B. Defects in the balance between GC-mediated and non-GC-mediated effects on PMCA1 expression may have adverse effects on neuronal function and ultimately result in irreversible neuronal damage.

L16 ANSWER 20 OF 38 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN DUPLICATE 5

ACCESSION NUMBER: 2000338890 EMBASE
TITLE: Cloning and functional expression of human retinal Kir2.4, a pH-sensitive inwardly rectifying K+ channel.
AUTHOR: Hughes B.A.; Kumar G.; Yuan Y.; Swaminathan A.; Yan D.; Sharma A.; Plumley L.; Yang-Feng T.L.; Swaroop A.
CORPORATE SOURCE: B.A. Hughes, Dept. of Ophthalmology, Univ. of Michigan, Kellogg Eye Center, 1000 Wall St., Ann Arbor, MI 48105, United States. bhughes@umich.edu
SOURCE: American Journal of Physiology - Cell Physiology, (2000) 279/3 48-3 (C771-C784). Refs: 56
ISSN: 0363-6143 CODEN: AJPCDD
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 002 Physiology

029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English
AB To identify novel potassium channel **genes** expressed in the retina, we **screened** a human retina cDNA library with an EST sequence showing partial homology to inwardly rectifying potassium (Kir) channel genes. The isolated cDNA yielded a 2,961-base pair sequence with the predicted open reading frame showing strong homology to the rat Kir2.4 (rKir2.4). Northern analysis of **mRNA** from human and bovine tissues showed preferential expression of Kir2.4 in the neural retina. In **situ hybridization** to sections of monkey retina detected Kir2.4 transcript in most retinal neurons. Somatic hybridization analysis and dual-color in **situ hybridization** to metaphase chromosomes mapped Kir2.4 to human chromosome 19 q13.1-q13.3. Expression of human Kir2.4 cRNA in Xenopus oocytes generated strong, inwardly rectifying K+ currents that were enhanced by extracellular alkalinization. We conclude that human Kir2.4 encodes an inwardly rectifying K + channel that is preferentially expressed in the neural retina and that is sensitive to physiological changes in extracellular pH.

=> d l16 ibib abs 21=30
'21=30' IS NOT VALID HERE
Your input could not be processed as entered. For more help, please enter "HELP DISPLAY UNIT" at an arrow prompt (=>).

=> d l16 ibib abs 21-30

L16 ANSWER 21 OF 38 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN
ACCESSION NUMBER: 2000069012 EMBASE
TITLE: Membrane fusion proteins are required for oskar **mRNA localization** in the Drosophila egg chamber.
AUTHOR: Ruden D.M.; Sollars V.; Wang X.; Mori D.; Alterman M.; Lu X.
CORPORATE SOURCE: D.M. Ruden, Department of Molecular Biosciences, University of Kansas, Lawrence, KS 66045, United States. ruden@eagle.cc.ukans.edu
SOURCE: Developmental Biology, (15 Feb 2000) 218/2 (314-325). Refs: 38
ISSN: 0012-1606 CODEN: DEBIAO
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English
AB We used a genetic screen in Drosophila to identify mutations which disrupt the **localization** of oskar **mRNA** during oogenesis. Based on the hypothesis that some cytoskeletal components which are required during the mitotic divisions will also be required for oskar **mRNA localization** during oogenesis, we designed the following genetic screen. We **screened** for P- element insertions in **genes** which slow down the blastoderm mitotic divisions. A secondary genetic screen was to generate female germ-line clones of these potential cell division cycle genes and to identify those which cause the mislocalization of oskar **mRNA**. We identified mutations in ter94 which disrupt the **localization** of oskar **mRNA** to the posterior pole of the oocyte. Ter94 is a member of the CDC48p/VCP subfamily of AAA proteins which are involved in homotypic fusion of the endoplasmic reticulum during mitosis. Consistent with the function of the yeast orthology ter94-mutant egg chambers are defective in the assembly of the endoplasmic reticulum. We tested whether other membrane biosynthesis genes are required for localizing oskar **mRNA** during oogenesis. We

found that ovaries that are mutant for syntaxin-1a, rop, and synaptotagmin are also defective in oskar **mRNA localization** during oogenesis. We suggest a pathway for the role of membrane assembly proteins on oskar **mRNA localization**. (C) 2000 Academic Press.

L16 ANSWER 22 OF 38 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.
on STN DUPLICATE 6

ACCESSION NUMBER: 2001005657 EMBASE
TITLE: Characterization of a Drosophila homologue of the human myelodysplasia/myeloid leukemia factor (MLF).
AUTHOR: Ohno K.; Takahashi Y.; Hirose F.; Inoue Y.H.; Taguchi O.; Nishida Y.; Matsukage A.; Yamaguchi M.
CORPORATE SOURCE: M. Yamaguchi, Division of Biochemistry, Aichi Cancer Ctr. Research Institute, Chikusa-ku, Nagoya 464-8681, Japan. myamaguc@aichi-cc.pref.aichi.jp
SOURCE: Gene, (30 Dec 2000) 260/1-2 (133-143).
Refs: 33
ISSN: 0378-1119 CODEN: GENED6
PUBLISHER IDENT.: S 0378-1119(00)00447-9
COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 022 Human Genetics
029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English

AB The transcription factor DREF regulates proliferation-related **genes** in Drosophila. With two-hybrid **screening** using DREF as a bait, we have obtained a clone encoding a protein homologous to human myelodysplasia/myeloid leukemia factor 1 (hMLF1). We termed the protein Drosophila MLF (dMLF); it consists of a polypeptide of 309 amino acid residues, whose sequence shares 23.1% identity with hMLF1. High conservation of 54.2% identity over 107 amino acids was found in the central region. The dMLF gene was mapped to 52D on the second chromosome by in **situ hybridization**. Interaction between dMLF and DREF in vitro could be confirmed by glutathione S-transferase pull-down assay, with the conserved central region appearing to play an important role in this. Northern blot hybridization analysis revealed dMLF **mRNA** levels to be high in unfertilized eggs, early embryos, pupae and adult males, and relatively low in adult females and larvae. This fluctuation of **mRNA** during Drosophila development is similar to that observed for DREF **mRNA**, except in the pupa and adult male. Using a specific antibody against the dMLF, we performed immunofluorescent staining of Drosophila Kc cells and showed a primarily cytoplasmic staining, whereas DREF localizes in the nucleus. However, dMLF protein contains a putative 14-3-3 binding motif involved in the subcellular **localization** of various regulatory molecules, and interaction with DREF could be regulated through this motif. The transgenic fly data suggesting the genetic interaction between DREF and dMLF support this possibility. Characterization of dMLF in the present study provides the molecular basis for analysis of its significance in Drosophila. .COPYRGT. 2000 Elsevier Science B.V.

L16 ANSWER 23 OF 38 MEDLINE on STN DUPLICATE 7

ACCESSION NUMBER: 2000122160 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10656923
TITLE: Coding sequence, chromosomal **localization**, and expression pattern of Nrf1: the mouse homolog of Drosophila erect wing.
AUTHOR: Schaefer L; Engman H; Miller J B
CORPORATE SOURCE: Myogenesis Research Laboratory, Massachusetts General Hospital, Charlestown 02129, USA.
SOURCE: Mammalian genome : official journal of the International Mammalian Genome Society, (2000 Feb) 11 (2) 104-10.
Journal code: 9100916. ISSN: 0938-8990.

PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200002
ENTRY DATE: Entered STN: 20000309
Last Updated on STN: 20000309
Entered Medline: 20000218

AB In Drosophila, the erect wing (ewg) protein is required for proper development of the central nervous system and the indirect flight muscles. The fly ewg gene encodes a novel DNA-binding domain that is also found in four genes previously identified in sea urchin, chicken, zebrafish, and human. To identify mouse ewg homologs, we designed degenerate primers to the conserved DNA-binding domain. The RT-PCR product obtained from **mRNA** of the mouse muscle cell line C2C12 was used to **screen** cDNA libraries; a single **gene** was identified which encodes a predicted 503 amino acid protein. The mouse ewg homolog, termed Nrf1, was mapped to proximal Chr 6. By RT-PCR and Northern analysis, Nrf1 was expressed in all tissues examined, and Northern analysis on adult tissues revealed a complex banding pattern suggesting extensive alternative splicing. Nrf1 hybridized to **mRNA** transcripts at approximately 2.2 kb, 4.0 kb, 4.4 kb, and 5.0 kb, with additional tissue-specific transcripts at 1.5 kb in testis, 1.9 kb in lung, and 3.7 kb in skeletal muscle. In **situ hybridization** on whole-mount E9-10.5 embryos showed a broad pattern of expression, with the highest levels of expression in the central nervous system, somites, first branchial arch, optic vesicle, and otic vesicle.

L16 ANSWER 24 OF 38 MEDLINE on STN DUPLICATE 8
ACCESSION NUMBER: 2000005540 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10537148
TITLE: Role of progesterone receptor activation in pituitary adenylate cyclase activating polypeptide gene expression in rat ovary.
AUTHOR: Ko C; In Y H; Park-Sarge O K
CORPORATE SOURCE: Department of Physiology, University of Kentucky, Lexington 40536-0084, USA.
CONTRACT NUMBER: HD-01135 (NICHD)
HD-30719 (NICHD)
HD-36879 (NICHD)
SOURCE: Endocrinology, (1999 Nov) 140 (11) 5185-94.
Journal code: 0375040. ISSN: 0013-7227.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
ENTRY MONTH: 199911
ENTRY DATE: Entered STN: 20000111
Last Updated on STN: 20000111
Entered Medline: 19991122

AB It is well known that the pituitary gonadotropin surge induces progesterone receptor (PR) gene expression in luteinizing granulosa cells and that PR activation is critical for successful ovulation. To further understand the molecular mechanism(s) by which PR plays a role critical for granulosa cell functions, we wanted to identify progesterone-induced genes in granulosa cells. We employed a PCR-based subtraction cloning strategy to **screen** for **genes** expressed differentially in granulosa cells that were challenged with forskolin in the presence of progesterone or ZK98299. One such differentially expressed clone was identified as the pituitary adenylate cyclase activating polypeptide (PACAP). To begin to understand the relationship between PR activation and PACAP gene expression in luteinizing granulosa cells, we examined whether PR and PACAP messenger RNA (**mRNA**) expression is

temporally correlated. In cultured granulosa cells, both human CG and forskolin induced PR and PACAP **mRNA** levels in a dose-dependent manner, as determined by semi-quantitative RT-PCR assays. However, the peak expression for PR and PACAP mRNAs was observed at 3 h and 6 h after hormone treatment, respectively. This time difference in cAMP-responsive expression of the PR and PACAP genes is due, at least in part, to the requirement of ongoing protein synthesis for PACAP expression, as demonstrated by the inhibitory effect of cycloheximide on cAMP-induced PACAP, but not PR, **mRNA** levels. To determine whether PR synthesis is prerequisite for PACAP expression, we examined the effect of ZK98299, a specific PR antagonist, on cAMP-induced PACAP **mRNA** expression. This compound blocked cAMP-induced PACAP **mRNA** expression in a dose-dependent manner, indicating that PR activation is required for PACAP gene expression in granulosa cells. We then compared cellular **localization** and hormonal regulation of ovarian PR and PACAP gene expression in immature rats treated with gonadotropins as well as in adult rats during the preovulatory period by using in **situ hybridization** and semiquantitative RT-PCR assays. Results show that both PR and PACAP mRNAs are induced in granulosa cells of preovulatory follicles by human CG, but that the PR gene is expressed before the PACAP gene. Taken together, these results demonstrate that PRs mediate the LH-induced PACAP gene expression in rat granulosa cells.

L16 ANSWER 25 OF 38 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
ACCESSION NUMBER: 1998:599725 SCISEARCH
THE GENUINE ARTICLE: 106AV
TITLE: Human mitochondrial phosphoenolpyruvate carboxykinase 2 gene - Structure, chromosomal **localization** and tissue-specific expression
AUTHOR: Modaressi S; Brechtel K; Christ B; Jungermann K (Reprint)
CORPORATE SOURCE: UNIV GOTTINGEN, INST BIOCHEM & MOL ZELLBIOL, HUMBOLDTALLEE 23, D-37073 GOTTINGEN, GERMANY (Reprint); UNIV GOTTINGEN, INST BIOCHEM & MOL ZELLBIOL, D-37073 GOTTINGEN, GERMANY
COUNTRY OF AUTHOR: GERMANY
SOURCE: BIOCHEMICAL JOURNAL, (15 JUL 1998) Vol. 333, Part 2, pp. 359-366.
Publisher: PORTLAND PRESS, 59 PORTLAND PLACE, LONDON W1N 3AJ, ENGLAND.
ISSN: 0264-6021.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: English
REFERENCE COUNT: 47

*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*

AB The mitochodrial (mt) phosphoenolpyruvate carboxykinase 2 (PCK2) **gene** was isolated by **screening** a human genomic library with a rat cytosolic (cy) PCK1 cDNA probe comprising sequences from exons 2-9 and by PCR amplification of human genomic DNA spanning consecutive exons with known primer pairs from mtPCK2 cDNA containing sequences from two putative neighbouring exons. The mtPCK2 gene spans approx. 10 kb and consists of ten exons and nine introns, All exon-intron junction sequences match the classical GT/AG rule. Northern blot analysis of poly(A)(+) and total RNA from various tissues revealed one **mRNA** species of approx. 2.4 kb. The gene is expressed in a variety of human tissues, mainly in liver, kidney, pancreas, intestine and fibroblasts. In contrast with the cytosolic isoenzyme, the mitochondrial form might not have a purely gluconeogenic function. The mtPCK2 gene maps to chromosome 14q11.2-q12, in contrast with the cyPCK1 gene located on 20q13.2-q13.31.

L16 ANSWER 26 OF 38 MEDLINE on STN DUPLICATE 9
ACCESSION NUMBER: 97307775 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9165117
TITLE: A vegetally localized T-box transcription factor in Xenopus eggs specifies mesoderm and endoderm and is essential for

embryonic mesoderm formation.
AUTHOR: Horb M E; Thomsen G H
CORPORATE SOURCE: Department of Biochemistry and Cell Biology, Institute for Cell and Developmental Biology, State University of New York, Stony Brook 11794-5215, USA.
SOURCE: Development (Cambridge, England), (1997 May) 124 (9) 1689-98.
Journal code: 8701744. ISSN: 0950-1991.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U89707
ENTRY MONTH: 199706
ENTRY DATE: Entered STN: 19970630
Last Updated on STN: 20030222
Entered Medline: 19970619

AB Pattern formation in early embryogenesis is guided by maternal, localized determinants and by inductive interactions between cells. In Xenopus eggs, localized molecules have been identified and some, such as Vg1 and Xwnt-11, can specify cell fates by functioning as inducers or patterning agents. We have used differential **screening** to identify new Xenopus **genes** that regulate mesodermal patterning, and we have isolated a new member of the T-box family of transcription factors. This gene, named Brat, is expressed maternally and its transcripts are localized to the vegetal hemisphere of the egg. During early embryonic cleavage, Brat **mRNA** becomes partitioned primarily within vegetal cells that are fated to form the endoderm. Zygotic expression of Brat begins at the onset of gastrulation within the presumptive mesoderm of the marginal zone. Consistent with its zygotic expression pattern, Brat induces, in a dose-dependent manner, a full spectrum of mesodermal genes that mark tissues across the dorsal-ventral axis, from the blood through the Spemann organizer. Brat also induces endoderm, consistent with its vegetal **localization**, making Brat a good candidate for a maternal determinant of the endoderm. We tested whether endogenous Brat is required for mesoderm formation by expressing a dominant-negative, transcriptional repressor form of Brat in embryos. This treatment inhibited mesoderm formation and severely disrupted normal development, thereby establishing that Brat plays a critical role in embryonic mesoderm formation and body patterning.

L16 ANSWER 27 OF 38 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
ACCESSION NUMBER: 1997:180376 BIOSIS
DOCUMENT NUMBER: PREV199799472089
TITLE: Cloning and chromosomal mapping of four putative novel human G-protein-coupled receptor genes.
AUTHOR(S): O'Dowd, Brian F. [Reprint author]; Nguyen, Tuan; Jung, Benjamin P.; Marchese, Adriano; Cheng, Regina; Heng, Henry H. Q.; Kolakowski., Lee F., Jr.; Lynch, Kevin R.; George, Susan R.
CORPORATE SOURCE: Dep. Pharmacol., Univ. Toronto, Toronto, ON M5S 1A8, Canada
SOURCE: Gene (Amsterdam), (1997) Vol. 187, No. 1, pp. 75-81.
CODEN: GENED6. ISSN: 0378-1119.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 24 Apr 1997
Last Updated on STN: 24 Apr 1997

AB We report the discovery of four novel human putative G-protein-coupled receptor (GPCR) genes. Gene GPR20 was isolated by amplifying genomic DNA with oligos based on the opioid and somatostatin related receptor **genes** and subsequent **screening** of a genomic library. Also, using our customized search procedure of a database of expressed sequence tags (dbEST), cDNA sequences that partially encoded novel GPCRs were identified. These cDNA fragments were obtained and used to screen a

genomic library to isolate the full-length coding region of the genes. This resulted in the isolation of genes GPR21, GPR22 and GPR23. The four encoded receptors share significant identity to each other and to other members of the receptor family. Northern blot analysis revealed expression of GPR20 and GPR22 in several human brain regions while GPR20 expression was detected also in liver. Fluorescence in **situ hybridization** (FISH) was used to map GPR20 to chromosome 8q, region 24.3-24.2, GPR21 to chromosome 9, region q33, GPR22 to chromosome 7, region q22-q31.1, and GPR23 to chromosome X, region q13-q21.1.

L16 ANSWER 28 OF 38 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
ACCESSION NUMBER: 97:57451 SCISEARCH
THE GENUINE ARTICLE: WB289
TITLE: The alpha 1 subunit of soluble guanylyl cyclase is expressed prenatally in the rat brain
AUTHOR: Smigrodzki R (Reprint); Levitt P
CORPORATE SOURCE: UNIV MED & DENT NEW JERSEY, ROBERT WOOD JOHNSON MED SCH, DEPT NEUROSCI & CELL BIOL, 675 HOES LANE, PISCATAWAY, NJ 08854 (Reprint)
COUNTRY OF AUTHOR: USA
SOURCE: DEVELOPMENTAL BRAIN RESEARCH, (23 DEC 1996) Vol. 97, No. 2, pp. 226-234.
Publisher: ELSEVIER SCIENCE BV, PO BOX 211, 1000 AE AMSTERDAM, NETHERLANDS.
ISSN: 0165-3806.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: English
REFERENCE COUNT: 28

*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*

AB The **mRNA** encoding the alpha 1 subunit of soluble guanylyl cyclase (alpha 1sGC) was identified in a differential-display **screening** for **genes** spatially and temporally regulated during the development of fetal rat brain. The initially isolated fragment of the 3' untranslated region was used for in **situ hybridization** and to produce full-length cDNA clones by hybridization screening of cDNA libraries and by RACE (rapid amplification of cDNA ends), respectively. In **situ hybridization** analysis revealed that alpha 1sGC wits absent at embryonic day 12 (E12), but by E14-E15, the forebrain exhibited dense expression in the developing striatum, medial cerebral wall containing the presumptive hippocampus, cerebellar neuroepithelium, and roof plate. Weaker expression was observed in the septum, epithalamus, ventral thalamus, pineal gland and retina. This pattern is largely maintained and refined at E18, with additional expression domains in the olfactory tubercle, nucleus accumbens, zona incerta and neocortex. During early postnatal development, the adult pattern is expressed, as previously reported. The unexpected, early expression of alpha 1sGC, in conjunction with the known absence of its heterodimeric partner, the beta subunit of sGC, from the developing rodent brain during fetal ages raises potentially novel functional roles of the alpha 1 subunit during ontogeny, and might imply the existence of an alternative beta subunit specific for the prenatal brain.

L16 ANSWER 29 OF 38 MEDLINE on STN DUPLICATE 10
ACCESSION NUMBER: 96044445 MEDLINE
DOCUMENT NUMBER: PubMed ID: 7558005
TITLE: Structure and chromosomal **localization** of a human water channel (AQP3) gene.
COMMENT: Erratum in: Genomics 1995 Dec 10;30(3):633
AUTHOR: Ishibashi K; Sasaki S; Saito F; Ikeuchi T; Marumo F
CORPORATE SOURCE: Second Department of Internal Medicine, School of Medicine, Tokyo, Japan.
SOURCE: Genomics, (1995 May 20) 27 (2) 352-4.
Journal code: 8800135. ISSN: 0888-7543.

PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-D25280
ENTRY MONTH: 199511
ENTRY DATE: Entered STN: 19951227
Last Updated on STN: 19980206
Entered Medline: 19951113

AB A cDNA encoding rat AQP3, a water channel and a member of the MIP family, that is expressed predominantly in kidney medulla and colon was cloned recently. To determine the structure, tissue distribution, and chromosomal **localization** of the human AQP3 **gene**, we **screened** a human kidney cDNA library with rat AQP3 probe and isolated a cDNA coding for human AQP3 protein. The deduced amino acid sequence of human AQP3 was 91% identical to rat AQP3. Human AQP3 **mRNA** was expressed in colon, kidney, liver, pancreas, lung, peripheral leukocytes, spleen, and prostate. The human AQP3 gene was mapped to 7q36.2-q36.3 by chromosome fluorescence in **situ hybridization**.

L16 ANSWER 30 OF 38 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
ACCESSION NUMBER: 95:106320 SCISEARCH
THE GENUINE ARTICLE: QE734
TITLE: THE HUMAN AND MOUSE HOMOLOGS OF THE YEAST RAD52 GENE - CDNA CLONING, SEQUENCE-ANALYSIS, ASSIGNMENT TO HUMAN-CHROMOSOME 12P12.2-P13, AND MESSENGER-RNA EXPRESSION IN MOUSE-TISSUES
AUTHOR: SHEN Z Y; DENISON K; LOBB R; GATEWOOD J M; CHEN D J (Reprint)
CORPORATE SOURCE: LOS ALAMOS NATL LAB, DIV LIFE SCI, LS-1, MS M888, LOS ALAMOS, NM, 87545 (Reprint); LOS ALAMOS NATL LAB, DIV LIFE SCI, LOS ALAMOS, NM, 87545
COUNTRY OF AUTHOR: USA
SOURCE: GENOMICS, (01 JAN 1995) Vol. 25, No. 1, pp. 199-206. ISSN: 0888-7543.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 40

*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*

AB The yeast Saccharomyces cerevisiae RAD52 gene is involved in DNA double strand break repair and mitotic/meiotic recombination. The N-terminal amino acid sequence of yeast S. cerevisiae, Schizosaccharomyces pombe, and Kluyveromyces lactis and chicken is highly conserved. Using the technology of mixed oligo nucleotide primed amplification of cDNA (MOPAC), two mouse RAD52 homologous cDNA fragments were amplified and sequenced. Subsequently, we have cloned the cDNA of the human and mouse homologs of yeast RAD52 **gene** by **screening** cDNA libraries using the identified mouse cDNA fragments. Sequence analysis of cDNA derived amino acid revealed a highly conserved N-terminus among human, mouse, chicken, and yeast RAD52 genes. The human RAD52 gene was assigned to chromosome 12p12.2-p13 by fluorescence in **situ hybridization**, R-banding, and DNA analysis of somatic cell hybrids. Unlike chicken RAD52 and mouse RAD51, no significant difference in mouse RAD52 **mRNA** level was found among mouse heart, brain, spleen, lung, liver, skeletal muscle, kidney, and testis. In addition to an similar to 1.9-kb RAD52 **mRNA** band that is present in all of the tested tissues, an extra **mRNA** species of similar to 0.85 kb was detectable in mouse testis. 

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